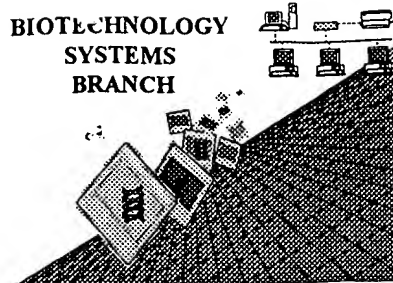


RAW SEQUENCE LISTING **ERROR REPORT**



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/836,911
Source: O/PE
Date Processed by STIC: 5/3/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

BEST AVAILABLE COPY

OIPE

RAW SEQUENCE LISTING DATE: 05/03/2001
 PATENT APPLICATION: US/09/836,911 TIME: 15:56:14

Input Set : A:\402iseq.001
 Output Set: N:\CRF3\05032001\I836911.raw

Does Not Comply
Corrected Diskette Needed

P.S

SEQUENCE LISTING

```

C--> 4 (1) GENERAL INFORMATION:
      6 (i) APPLICANT: Hadlaczky, Gyula
      7 Szalay, Aladar
C--> 9 (ii) TITLE OF INVENTION: ARTIFICIAL CHROMOSOMES, USES THEREOF
      10 AND METHODS FOR PREPARING ARTIFICIAL CHROMOSOMES
      12 (iii) NUMBER OF SEQUENCES: 34
      14 (iv) CORRESPONDENCE ADDRESS:
      15 (A) ADDRESSEE: Heller Ehrman White & McAuliffe
      16 (B) STREET: 4350 La Jolla Village Drive, 6th Floor
      17 (C) CITY: San Diego
      18 (D) STATE: CA
      19 (E) COUNTRY: USA
      20 (F) ZIP: 92122
      22 (v) COMPUTER READABLE FORM:
      23 (A) MEDIUM TYPE: Diskette
      24 (B) COMPUTER: IBM Compatible
      25 (C) OPERATING SYSTEM: DOS
      26 (D) SOFTWARE: FastSEQ Version 1.5
      28 (vi) CURRENT APPLICATION DATA:
C--> 29 (A) APPLICATION NUMBER: US/09/836,911
C--> 30 (B) FILING DATE: 17-Apr-2001
      50 (C) CLASSIFICATION:
C--> 47 (vii) PRIOR APPLICATION DATA:
      33 (A) APPLICATION NUMBER: 08/835,682
      34 (B) FILING DATE: 10-APR-1997
      38 (A) APPLICATION NUMBER: 08/695,191
      39 (B) FILING DATE: 07-AUG-1996
      43 (A) APPLICATION NUMBER: 08/682,080
      44 (B) FILING DATE: 15-JUL-1996
      48 (A) APPLICATION NUMBER: 08/629,822
      49 (B) FILING DATE: 10-APR-1996
      52 (viii) ATTORNEY/AGENT INFORMATION:
      53 (A) NAME: Seidman, Stephanie L
      54 (B) REGISTRATION NUMBER: 33,779
      55 (C) REFERENCE/DOCKET NUMBER: 24601-402I
      58 (ix) TELECOMMUNICATION INFORMATION:
      59 (A) TELEPHONE: 858-450-8403
      60 (B) TELEFAX: 858-587-5360
      61 (C) TELEX:
      63 (2) INFORMATION FOR SEQ ID NO: 1:
      65 (i) SEQUENCE CHARACTERISTICS:
      66 (A) LENGTH: 1293 base pairs
      67 (B) TYPE: nucleic acid
      68 (C) STRANDEDNESS: single
      69 (D) TOPOLOGY: linear
      71 (ii) MOLECULE TYPE: Genomic DNA
  
```

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/836,911

DATE: 05/03/2001

TIME: 15:56:14

Input Set : A:\402iseq.001

Output Set: N:\CRF3\05032001\I836911.raw

```

72      (iii) HYPOTHETICAL: NO
C--> 73      (iv) ANTI-SENSE: NO
W--> 74      (v) FRAGMENT TYPE:
75      (vi) ORIGINAL SOURCE:
76      (ix) FEATURE:
78      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
80      GAATTCATCA TTTTTCANGT CCTCAAGTGG ATGTTTCTCA TTNCCATGA TTTTAAGTTT      60
81      TCTCGCCATA TTCCTGGTCC TACAGTGGGC ATTTCTCCAT TTNACAGTT TTNCAGTGAT      120
82      TTCGTCAATT TCAAGTCCTC AAGTGGATGT TTCTCATTTN CCATGAATTT CAGTTTTCNTN      180
83      GCCATATTCC ACGTCCTACA GNGGACATTT CTAAATTTNC CACCTTTTTT AGTTTTCCTC      240
84      GCCATATTTC ACGTCCTAAA ATGTGTATTT CTCGTTTNCC GTGATTTTCA GTTTTCTCGC      300
85      CAGATTCCAG GTCCTATAAT GTGCATTCTT CATTTNNCAC GTTTTTCAGT GATTTCGTCA      360
86      TTTTTTCAAG TCGGCAAGTG GATGTTTCTC ATTTNCCATG ATTTNCAGTT TTCTTGNAAT      420
87      ATTCCATGTC CTACAATGAT CATTTTTAAT TTTCCACCTT TTCATTTTTT CACGCCATAT      480
88      TTCATGTCCT AAAGTGTATA TTTCTCCTTT TCCGCGATTT TCAGTTTCTT CGCCATATTC      540
89      CAGGTGCTAC AGTGTGCATT CCTCATTTT CACCTTTTTT ACTGATTTCG TCATTTTTTCA      600
90      AGTCGTCAAC TGGATCTTTC TAATTTTCCA TGATTTTTCAG TTATCTTGTC ATATTCCATG      660
91      TCCTACAGTG GACATTTCTA AATTTTCCAA CTTTTTCAAT TTTTCTCGAC ATATTGACG      720
92      TGCTAAAGTG TGTATTTCTT ATTTTCCGTG ATTTTCAGTT TTCTCGCCAT ATTCCAGGTC      780
93      CTAATAGTGT GCATTTCTCA TTTTTCACGT TTTTCAGTGA TTTTCGTCATT TTTTCCAGTT      840
94      GTCAAGGGGA TGTTCCTCAT TTTCCATGAG TGTCAGTTT CTGCTATAT TCCATGTCCT      900
95      ACAGTGACAT TTCTAAATAT TATACCTTTT TCAGTTTTC TCACCATATT TCACGTCCTA      960
96      AAGTATATAT TTCTCATTTT CCCTGATTTT CAGTTTCCTT GCCATATTCC AGGTCCTACA      1020
97      GTGTGCATTT CTCATTTTTC ACGTTTTCCTA GTAATTTCTT CATTTTTTTAA GCCCTCAAAT      1080
98      GGATGTTTCT CATTTTCCAT GATTTTCAGT TTTCTTGCCA TATACCATGT CCTACAGTGG      1140
99      ACATTTCTAA ATTATCCACC TTTTTCAGTT TTTTCATCGG ACATTTTCAG TCCTAAAGTG      1200
100     TGTATTTCTA ATTTTCAGTG ATTTTCAGTT TTCTCGCCAT ATTCCAGGAC CTACAGTGTG      1260
101     CATTTCTCAT TTTTCACGTT TTTTCAGTGA TTC      1293
103 (2) INFORMATION FOR SEQ ID NO: 2:
105     (i) SEQUENCE CHARACTERISTICS:
106         (A) LENGTH: 1044 base pairs
107         (B) TYPE: nucleic acid
108         (C) STRANDEDNESS: single
109         (D) TOPOLOGY: linear
111     (ii) MOLECULE TYPE: Genomic DNA
112     (iii) HYPOTHETICAL: NO
C--> 113     (iv) ANTI-SENSE: NO
W--> 114     (v) FRAGMENT TYPE:
115     (vi) ORIGINAL SOURCE:
116     (ix) FEATURE:
118     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
120     AGGCCTATGG TGA AAAAGGA AATATCTTCC CTGAAAACCT AGACAGAAGG ATTCTCAGAA      60
121     TCTTATTTGT GATGTGCGCC CCTCAACTAA CAGTGTGAA GCTTTCTTTT GATAGAGCAG      120
122     TTTTGAAACA CTCTTTTGT AAAATCTGCA AGAGGATATT TGGATAGCTT TGAGGATTTC      180
123     CGTTGGAAAC GGGATGTCT TCATATAAAC CCTAGACAGA AGCATTCTCA GAAGCTTCAT      240
124     TGGGATGTTT CAGTTGAAGT CACAGTGTG AACAGTCCCC TTTCATAGAG CAGGTTTGAA      300
125     ACACTCTTTT TTGTAGTATC TGGGAAGTGA CATTGGAGC GATCTCAGGA CTGCGGTGAA      360
126     AAAGGAAATA TCTTCCAATA AAAGCTAGAT AGAGGCAATG TCAGAAACCT TTTTCATGAT      420
127     GTATCTACTC AGCTAACAGA GTTGAACCTT CCTTTGAGAG AGCAGTTTTG AAACACTCTT      480

```

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/836,911

DATE: 05/03/2001

TIME: 15:56:14

Input Set : A:\402iseq.001

Output Set: N:\CRF3\05032001\I836911.raw

```

128 TTTGTGGAAT CTGCAAGTGG ATATTTGTCT AGCTTTGAGG ATTTTCGTTGG GAAACGGGAT 540
129 TACATATAAA AAGCAGACAG CAGCATTCCT AGAACTTCT TTGTGATGTT TGCATTCAAG 600
130 TCACAGAGTT GAACATTCCC TTTCATAGAG CAGGTTTGAA ACACACTTTT TGATGTATCT 660
131 GGATGTGGAC ATTTGCAGCG CTTTCAGGCC TAAGTGAAA AGGAAATATC TTCCCCTGAA 720
132 AACTAGACAG AAGCATTCTC AGAACTTAT TTGTGATGTG CGCCCTCAAC TAACAGTGT 780
133 GAAGCTTTCT TTTGATAGAG GCAGTTTGA AACACTCTTT TGTGGAATCT GCAAGTGGAT 840
134 ATTTGTCTAG CTTTGAGGAT TTCTTTGGAA ACGGGATTAC ATATAAAAAG CAGACAGCAG 900
135 CATTCCCAGA ATCTTGTTTG TGATGTTTGC ATTCAAGTCA CAGAGTTGAA CATTCCCTTT 960
136 CAGAGAGCAG GTTTGAACAC TCTTTTATA GTATCTGGAT GTGGACATTT GGAGCGCTTT 1020
137 CAGGGGGGAT CCTCTAGAAT TCCT 1044

```

141 (2) INFORMATION FOR SEQ ID NO: 3:

143 (i) SEQUENCE CHARACTERISTICS:

144 (A) LENGTH: 2492 base pairs

145 (B) TYPE: nucleic acid

146 (C) STRANDEDNESS: single

147 (D) TOPOLOGY: linear

149 (ii) MOLECULE TYPE: Genomic DNA

150 (iii) HYPOTHETICAL: NO

C--> 151 (iv) ANTI-SENSE: NO

W--> 152 (v) FRAGMENT TYPE:

153 (vi) ORIGINAL SOURCE:

154 (ix) FEATURE:

156 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

```

158 CTGCAGCTGG GGGTCTCCAA TCAGGCAGGG GCCCTTACT ACTCAGATGG GGTGGCCGAG 60
159 TAGGGGAAGG GGGTGCAGGC TGCATGAGTG GACACAGCTG TAGGACTACC TGGGGGCTGT 120
160 GGATCTATGG GGGTGGGGAG AAGCCAGTG ACAGTGCCTA GAAGAGACAA GGTGGCCTGA 180
161 GAGGGTCTGA GGAACATAGA GCTGGCCATG TTGGGGCCAG GTCTCAAGCA GGAAGTGAGG 240
162 AATGGGACAG GCTTGAGGAT ACTCTACTCA GTAGCCAGGA TAGCAAGGAG GGCTTGGGGT 300
163 TGCTATCCTG GGGTTCAACC CCCAGGTTG AAGGCCCTGG GGGAGATGGT CCCAGGACAT 360
164 ATTACAATGG ACACAGGAGG TTGGGACACC TGGAGTCACC AAACAAAACC ATGCCAAGAG 420
165 AGACCATGAG TAGGGGTGTC CAGTCCAGCC CTCTGACTGA GCTGCATTGT TCAAATCCAA 480
166 AGGGCCCTG CTGCCACCTA GTGGCTGATG GCATCCACAT GACCCTGGGC CACACGCGTT 540
167 TAGGGTCTCT GTGAAGACCA AGATCCTTGT TACATTGAAC GACTCCTAAA TGAGCAGAGA 600
168 TTTCCACCTA TTCGAAACAA TCACATAAAA TCCATCCTGG AAAAAGCCTG GGGGATGGCA 660
169 CTAAGGCTAG GGATAGGGTG GGATGAAGAT TATAGTTACA GTAAGGGGTT TAGGGTTAGG 720
170 GATCAACGTT GGTTAGGAGT TAGGGATACA GTAGGGTACC GGTAGGGTTA GGGGTTAGGG 780
171 TTAGGGGTTA GGGTTAGGGT TAGGGTTAGG GTTAGGGTTA GGGGTTAGGG GTTAGGGTTA 840
172 GGGTTAGGTT TTGGGGTGGC GTATTTTGGT CTTATACGCT GTGTTCCACT GGCAATGAAA 900
173 AGAGTTCCTG TTTTTCCTTC AGCAATTTGT CATTTTTTAA AGAGTTTAGC AATTCTAACA 960
174 GATATAGACC AGCTGTGCTA TCTCATTGTG GTTTTCAATT GTAACCACAT TGTGGTTTCA 1020
175 ATGTGTTTAC TTGCCATCTG TAGATCTTCT TTGCGTGAGG TGTCTGTTCA GATGTGTGTG 1080
176 CATTTCCTGN NTTTTNGCTG TTTAACTTAT TGTTTAGTTT TAATAATTTT TTATATATTT 1140
177 GAAGACAAAT CTTTCTCAGA TGTGTATTTG CAAATATTTT TTCAATATGA GGCTTGCTTT 1200
178 TGTCTCTAAC AAGGTCTCTT CAGAGATAAC TTAATATAA GAAATCCACA CTGTCACTTC 1260
179 TTTTGTGTAT ATCTACCTTT TGTGTCATTT GTTAAATTC ATTACCAAAC CCAAAGGCAG 1320
180 ATAGCTTTTC TTCTATTGTT TCTTCTAGAA ATTTGTATAG TTTTGCATTT TTAGTGTAAG 1380
181 GATGATTTTG AGTGATTATT TGTGTAAGTT GTAAAGTTTT CGTCTATATC CATATCATTT 1440
182 CTTATGGTTT CCAATTAATC GTTCCCTCAC TATTTTGGG AAAGACACAG GATAGTGGGC 1500
183 TTTGTTAGAG TAGATAGGTA GCTAGACATG AACAGGAGGG GGCCTCCTGG AAAAGGGAAA 1560

```

RAW SEQUENCE LISTING

DATE: 05/03/2001

PATENT APPLICATION: US/09/836,911

TIME: 15:56:14

Input Set : A:\402iseq.001

Output Set: N:\CRF3\05032001\I836911.raw

```

184 GTCTGGGAAG GCTCACCTGG AGGACCACCA AAAATTCACA TATTAGTAGC ATCTCTAGTG 1620
185 CTGGAGTGGA TGGGCACTTG TCAATTGTGG GTAGGAGGGA AAAGAGGTCC TATGCAGAAA 1680
186 GAAACTCCCT AGAACTCTC TGAAAGATGCC CCAATCATTG ACTCTGCAAT AAAAATGTCA 1740
187 GAATATTGCT AGCTACATGC TGATAAGGNN AAAGGGGACA TTCTTAAGTG AAACCTGGCA 1800
188 CCATAAGTAC AGATTAGGGC AGAGAAGGAC ATTCAAAAGA GGCAGGCGCA GTAGGTACAA 1860
189 ACGTGATCGC TGTCAGTGTG CCTGGGATGG CGGGAAGGAG GCTGGTGCCA GAGTGGATTC 1920
190 GTATTGATCA CCACACATAT ACCTCAACCA ACAGTGAGGA GGTCACACAA GCCTAAGTGG 1980
191 GGCAAGTTGG GGAGCTAAGG CAGTAGCAGG AAAACCAGAC AAAGAAAACA GGTGGAGACT 2040
192 TGAGACAGAG GCAGGAATGT GAAGAAATCC AAAATAAAAT TCCCTGCACA GGAATCTTAG 2100
193 GCTGTTTAAAT GCATCGCTCA GTCCCACTCC TCCCTATTTT TCTACAATAA ACTCTTTACA 2160
194 CTGTGTTTCT TTTCAATGAA GTTATCTGCC ATCTTTGTAT TGCCTCTTGG TGAAAATGTT 2220
195 TCTTCCAAGT TAAACAAGAA CTGGGACATC AGCTCTCCCC AGTAATAGCT CCGTTTCAGT 2280
196 TTGAATTTAC AGAACTGATG GGCTTAATAA CTGGCGCTCT GACTTTAGTG GTGCAGGAGG 2340
197 CCGTCACACC GGGACCAAGA GTGCCCTGCC TAGTCCCCAT CTGCCCGCAG GTGGCGGCTG 2400
198 CCTCGACACT GACAGCAATA GGGTCCGGCA GTGTCCCCAG CTGCCAGCAG GGGGCGTACC 2460
199 ACGACTACAC TGTGAGCAAG AGGGCCCTG AG 2492

201 (2) INFORMATION FOR SEQ ID NO: 4:
203     (i) SEQUENCE CHARACTERISTICS:
204         (A) LENGTH: 28 base pairs
205         (B) TYPE: nucleic acid
206         (C) STRANDEDNESS: single
207         (D) TOPOLOGY: linear
209     (ii) MOLECULE TYPE: Genomic DNA
210     (iii) HYPOTHETICAL: NO
C--> 211     (iv) ANTI-SENSE: NO
W--> 212     (v) FRAGMENT TYPE:
213     (vi) ORIGINAL SOURCE:
214     (ix) FEATURE:
216     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
218 GGGGAATTCA TTGGGATGTT TCAGTTGA 28
220 (2) INFORMATION FOR SEQ ID NO: 5:
222     (i) SEQUENCE CHARACTERISTICS:
223         (A) LENGTH: 29 base pairs
224         (B) TYPE: nucleic acid
225         (C) STRANDEDNESS: single
226         (D) TOPOLOGY: linear
228     (ii) MOLECULE TYPE: Genomic DNA
229     (iii) HYPOTHETICAL: NO
C--> 230     (iv) ANTI-SENSE: NO
W--> 231     (v) FRAGMENT TYPE:
232     (vi) ORIGINAL SOURCE:
233     (ix) FEATURE:
235     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
237 CGAAAGTCCC CCCTAGGAGA TCTTAAGGA 29
239 (2) INFORMATION FOR SEQ ID NO: 6:
241     (i) SEQUENCE CHARACTERISTICS:
242         (A) LENGTH: 47 base pairs
243         (B) TYPE: nucleic acid
244         (C) STRANDEDNESS: single

```

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/836,911

DATE: 05/03/2001

TIME: 15:56:14

Input Set : A:\402iseq.001

Output Set: N:\CRF3\05032001\I836911.raw

```

245      (D) TOPOLOGY: linear
W--> 247      (ii) MOLECULE TYPE: DNA
248      (iii) HYPOTHETICAL: NO
C--> 249      (iv) ANTI-SENSE: NO
W--> 250      (v) FRAGMENT TYPE:
251      (vi) ORIGINAL SOURCE:
252      (ix) FEATURE:
254      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
256 CCGCTTAATA CTCTGATGAG TCCGTGAGGA CGAAACGCTC TCGCACC 47
260 (2) INFORMATION FOR SEQ ID NO: 7:
262      (i) SEQUENCE CHARACTERISTICS:
263          (A) LENGTH: 25 base pairs
264          (B) TYPE: nucleic acid
265          (C) STRANDEDNESS: single
266          (D) TOPOLOGY: linear
268      (ii) MOLECULE TYPE: Genomic DNA
269      (iii) HYPOTHETICAL: NO
C--> 270      (iv) ANTI-SENSE: NO
W--> 271      (v) FRAGMENT TYPE:
272      (vi) ORIGINAL SOURCE:
273      (ix) FEATURE:
275      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
277 CGATTTAAT TAATTAAGCC CGGGC 25
280 (2) INFORMATION FOR SEQ ID NO: 8:
282      (i) SEQUENCE CHARACTERISTICS:
283          (A) LENGTH: 27 base pairs
284          (B) TYPE: nucleic acid
285          (C) STRANDEDNESS: single
286          (D) TOPOLOGY: linear
288      (ii) MOLECULE TYPE: Genomic DNA
289      (iii) HYPOTHETICAL: NO
C--> 290      (iv) ANTI-SENSE: NO
W--> 291      (v) FRAGMENT TYPE:
292      (vi) ORIGINAL SOURCE:
293      (ix) FEATURE:
295      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
297 TAAATTTAAT TAATTCGGGC CCGTCGA 27
299 (2) INFORMATION FOR SEQ ID NO: 9:
301      (i) SEQUENCE CHARACTERISTICS:
302          (A) LENGTH: 69 base pairs
303          (B) TYPE: nucleic acid
304          (C) STRANDEDNESS: single
305          (D) TOPOLOGY: linear
307      (ii) MOLECULE TYPE: Genomic DNA
310      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
312 ATG TAC AGG ATG CAA CTC CTG TCT TGC ATT GCA CTA AGT CTT GCA CTT 48
313 Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu
W--> 315 GTC ACA AAC AGT GCA CCT ACT 69
316 Val Thr Asn Ser Ala Pro Thr

```

Please edit all subsequent sequences
containing these errors

(Per
Sequence Rules)

Number
the
amino
acids

Under every
5 amino
acids — do not
use TAB codes
between numbers 5/3/01

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/836,911

DATE: 05/03/2001

TIME: 15:56:15

Input Set : A:\402iseg.001

Output Set: N:\CRF3\05032001\I836911.raw

L:4 M:220 C: Keyword misspelled or invalid format, [(1) GENERAL INFORMATION:]
L:9 M:220 C: Keyword misspelled or invalid format, [(ii) TITLE OF INVENTION:]
L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:37 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]
L:42 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]
L:47 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]
L:73 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:78 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=1
L:74 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=1
L:113 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:118 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=2
L:114 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=2
L:151 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:156 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=3
L:152 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=3
L:211 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:216 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=4
L:212 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=4
L:230 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:235 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=5
L:231 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=5
L:249 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:254 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=6
L:247 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=6
L:250 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=6
L:270 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:275 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=7
L:271 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=7
L:290 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:295 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=8
L:291 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=8
L:308 M:220 C: Keyword misspelled or invalid format, [(D) OTHER INFORMATION:]
L:308 M:220 C: Keyword misspelled or invalid format, Poss data loss, Seq 9, (D) OTHER INFORMATION:
L:315 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:339 M:220 C: Keyword misspelled or invalid format, [(H) DOCUMENT NUMBER:]
L:433 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:438 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=11
L:434 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=11
L:452 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:457 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=12
L:453 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=12
L:471 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:472 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=13
L:512 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:513 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=14
L:553 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:554 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=15

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/836,911

DATE: 05/03/2001

TIME: 15:56:15

Input Set : A:\402iseq.001

Output Set: N:\CRF3\05032001\I836911.raw

L:593 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:594 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=16
L:979 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:980 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=17
L:1713 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1714 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=18
L:1734 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1735 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=19
L:1764 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1765 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=20
L:1789 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1790 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=21
L:1813 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1814 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=22
L:1837 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1838 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=23
L:1866 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1867 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=24
L:1896 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1897 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=25
L:1914 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1915 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=26
L:1932 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1933 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=27
L:1950 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1951 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=28
L:1968 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1969 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=29
L:1987 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1988 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=30
L:2005 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2006 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=31
L:2023 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2024 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=32
L:2041 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2042 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=33
L:2059 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2060 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=34